SEQUENCE LISTING

<110> THE SALK INSTITUTE FOR BIOLOGICAL STUDIES THE REGENTS OF THE UNIVERSITY OF CALIFORNIA LILJEGREN, Sarah, Jean ECKER, Joseph, R. YANOFSKY, Martin, F. <120> GENETIC CONTROL OF ORGAN ABSCISSION <130> SALKINS.035C1 <150> US 60/264,974 <151> 2001-01-29 <150> PCTUS02/01938 <151> 2002-01-22 <160> 21 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 1452 <212> DNA <213> Arabidopsis thaliana <220> <221> CDS <222> (1) . . . (1452) <400> 1 atg aac gag aaa gcc aac gtc tct aag gag ctt aat gcc cgc cat aga Met Asn Glu Lys Ala Asn Val Ser Lys Glu Leu Asn Ala Arg His Arg 10 aag att ctt gaa ggg ctt ctt aaa cat cca gag aac aga gaa tgt gct 96 Lys Ile Leu Glu Gly Leu Leu Lys His Pro Glu Asn Arg Glu Cys Ala 25 gac tgc aaa aca aaa ggt cca aga tgg gct agt gtt aat tta ggt atc 144 Asp Cys Lys Thr Lys Gly Pro Arg Trp Ala Ser Val Asn Leu Gly Ile 35 40 ttt atc tgc atg caa tgt tct ggg att cac agg agt ctc ggg gta cac 192 Phe Ile Cys Met Gln Cys Ser Gly Ile His Arg Ser Leu Gly Val His 50 55 ata tcg aag gtt cga tct gcc act ctg gac aca tgg ctc ccc gag cag 240 Ile Ser Lys Val Arg Ser Ala Thr Leu Asp Thr Trp Leu Pro Glu Gln 65 70

90

288

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Val Ala Phe Ile Gln Ser Met Gly Asn Asp Lys Ala Asn Ser Tyr Trp

| | | | cca Pro | | | | | | | | | | 336 |
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| | | | aaa Lys | | | | | | | | | | 528 |
| | | | ata Ile | | | | | | | | | | 576 |
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| | | | act Thr 230 | | | | | | | | | | 720 |
| | | | tca Ser | - | | | | _ | | | _ | _ | 768 |
| | | | ggc Gly | | | | | | | | | | 816 |
| | | | gcc Ala | | | | | | | | | | 864 |
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| | acg Thr | | | | | | | | 1008 |
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| | aac Asn | | | | | | | | 1248 |
| | gag Glu | | | | | | | | 1296 |
| | gct Ala 435 | | _ | _ | _ | | | | 1344 |
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| | | | | | | | | cca Pro | | | | | 96 |
| | | | | | | | | gct Ala | | | | | 144 |
| | | | | | | | | cac His | | | | | 192 |
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| - | - | | | | | | _ | aga Arg | _ | | | | 336 |
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180 185 190

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| | | | | | | | | | | | | | atg Met | | | 720 |
| | | | | | | | | | | | | | cct Pro | | | 768 |
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| tca Ser | tct Ser 290 | tct Ser | gac Asp | ttt Phe | gag Glu | gat Asp 295 | ttg Leu | ttt Phe | aag Lys | gac Asp | aca Thr 300 | cct Pro | aat Asn | tta Leu | aca Thr | 912 |
| act Thr 305 | caa Gln | caa Gln | gca Ala | cca Pro | aaa Lys 310 | gat Asp | gtg Val | aaa Lys | ggc Gly | gat Asp 315 | atc Ile | atg Met | agc Ser | ctg Leu | ttt Phe 320 | 960 |
| gag Glu | aag Lys | acg Thr | aat Asn | ata Ile 325 | gta Val | tcg Ser | cct Pro | ttt Phe | gcc Ala 330 | atg Met | cat His | cag Gln | caa Gln | cag Gln 335 | gtt Val | 1008 |
| | | | | | | | | | | | | | gcg Ala 350 | | | 1056 |
| gct Ala | gga Gly | ggc Gly 355 | act Thr | cca Pro | aac Asn | ggc Gly | gtg Val 360 | aat Asn | caa Gln | caa Gln | gct Ala | att Ile 365 | gct Ala | aat Asn | gct Ala | 1104 |
| ctt Leu | aac Asn 370 | gta Val | gct Ala | tct Ser | gca Ala | aat Asn 375 | tgg Trp | tca Ser | aac Asn | ccc Pro | ggc Gly 380 | ggc Gly | tac Tyr | cag Gln | atc Ile | 1152 |
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| ccg caa gag Pro Gln Glu | aac act Asn Thr 420 | cta caa Leu Gln | Tyr P | ca tca ro Ser 25 | tcc agt Ser Sei | ttc Phe | tac Tyr 430 | aca Thr | atg Met | 1296 |
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| cct cag tca Pro Gln Ser 450 | tca tcc Ser Ser | gca acc Ala Thr 455 | caa c Gln P | ca aca Pro Thr | agc acc Ser Th: | r Thr | cca Pro | tct Ser | tca Ser | 1392 |
| caa tca ggo Gln Ser Gly 465 | aaa gac Lys Asp | ttt gat Phe Asp 470 | ttc t Phe S | ct tcc er Ser | ttg atg Leu Me 475 | g gat E Asp | gga Gly | atg Met | ttc Phe 480 | 1440 |
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| Lys Val As | p Phe Ala | | | Phe Asn | Met Le | u Ser | Met | Asp | Asp | |

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